

L9	1	l8 and (fulgidus)	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/06/16 12:22
L10	2	("20030049643").PN.	US-PGPUB; USPAT; USOCR; EPO; DERWENT	OR	OFF	2005/06/16 12:23
L11	2	("20030049634").PN.	US-PGPUB; USPAT; USOCR; EPO; DERWENT	OR	OFF	2005/06/16 12:25
L12	2	("5556772").PN.	US-PGPUB; USPAT; USOCR; EPO; DERWENT	OR	OFF	2005/06/16 12:25
S1	2	("6713071").PN.	US-PGPUB; USPAT; USOCR; EPO; DERWENT	OR	OFF	2005/06/15 19:01
S2	2	("4693980").PN.	US-PGPUB; USPAT; USOCR; EPO; DERWENT	OR	OFF	2005/06/15 19:02
S3	2	("6881559").PN.	US-PGPUB; USPAT; USOCR; EPO; DERWENT	OR	OFF	2005/06/15 19:02
S4	2	("5453372").PN.	US-PGPUB; USPAT; USOCR; EPO; DERWENT	OR	OFF	2005/06/16 11:02

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	7672	exonuclease same polymerase	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/16 11:03
L2	37	I1 and ((enhanc\$4 fidelity increas\$) near exonuclease)	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/16 11:38
L3	15	I2 and ((composition combination) same (exonuclease))	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/16 11:48
L4	2	("6482590").PN.	US-PGPUB; USPAT; USOCR; EPO; DERWENT	OR	OFF	2005/06/16 11:49
L5	1502	(composition mixture combination) near5 (polymerase and exonuclease)	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/16 11:50
L6	0	I5 and fulgidis	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/16 11:50
L7	39	I5 and fulgidus	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/16 11:51
L8	2	("5843669").PN.	US-PGPUB; USPAT; USOCR; EPO; DERWENT	OR	OFF	2005/06/16 11:52

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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:18:10 ; Search time 157 Seconds
(without alignments)
628.553 Million cell updates/sec

Title: US-09-856-850A-18
Perfect score: 257
Sequence: 1 MLKIATFNVNSIRSRLHIVI.....KPRLAEKPSDHLPLVAVFDV 257

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1714042 seqs, 383979560 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:12:09 ; Search time 488 Seconds
(without alignments)
615.118 Million cell updates/sec

Title: US-09-856-850A-18
Perfect score: 257
Sequence: 1 MLKIATFNVNSIRSRLHIVI.....KPRLAEKPSDHLPLVAVFDV 257

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 6959266 seqs, 1168006243 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

- 1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*
- 2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*
- 3: /cgn2_6/ptodata/1/paa/US07_COMB.pep:*
- 4: /cgn2_6/ptodata/1/paa/US080_COMB.pep:*
- 5: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
- 6: /cgn2_6/ptodata/1/paa/US082_COMB.pep:*
- 7: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
- 8: /cgn2_6/ptodata/1/paa/US084_COMB.pep:*
- 9: /cgn2_6/ptodata/1/paa/US085_COMB.pep:*
- 10: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
- 11: /cgn2_6/ptodata/1/paa/US087_COMB.pep:*
- 12: /cgn2_6/ptodata/1/paa/US088_COMB.pep:*
- 13: /cgn2_6/ptodata/1/paa/US089_COMB.pep:*
- 14: /cgn2_6/ptodata/1/paa/US090_COMB.pep:*
- 15: /cgn2_6/ptodata/1/paa/US091_COMB.pep:*
- 16: /cgn2_6/ptodata/1/paa/US092_COMB.pep:*
- 17: /cgn2_6/ptodata/1/paa/US093_COMB.pep:*
- 18: /cgn2_6/ptodata/1/paa/US094_COMB.pep:*
- 19: /cgn2_6/ptodata/1/paa/US095_COMB.pep:*
- 20: /cgn2_6/ptodata/1/paa/US096_COMB.pep:*
- 21: /cgn2_6/ptodata/1/paa/US097A_COMB.pep:*
- 22: /cgn2_6/ptodata/1/paa/US097B_COMB.pep:*
- 23: /cgn2_6/ptodata/1/paa/US098_COMB.pep:*
- 24: /cgn2_6/ptodata/1/paa/US099A_COMB.pep:*
- 25: /cgn2_6/ptodata/1/paa/US099B_COMB.pep:*
- 26: /cgn2_6/ptodata/1/paa/US100_COMB.pep:*
- 27: /cgn2_6/ptodata/1/paa/US101_COMB.pep:*
- 28: /cgn2_6/ptodata/1/paa/US102_COMB.pep:*
- 29: /cgn2_6/ptodata/1/paa/US103_COMB.pep:*
- 30: /cgn2_6/ptodata/1/paa/US104_COMB.pep:*
- 31: /cgn2_6/ptodata/1/paa/US105_COMB.pep:*
- 32: /cgn2_6/ptodata/1/paa/US106_COMB.pep:*
- 33: /cgn2_6/ptodata/1/paa/US107_COMB.pep:*
- 34: /cgn2_6/ptodata/1/paa/US108_COMB.pep:*

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35: /cgn2_6/ptodata/1/paa/US109_COMB.pep:*
36: /cgn2_6/ptodata/1/paa/US110_COMB.pep:*
37: /cgn2_6/ptodata/1/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:14:59 ; Search time 60 Seconds
(without alignments)
526.230 Million cell updates/sec

Title: US-09-856-850A-18
Perfect score: 257
Sequence: 1 MLKIATFNVNSIRSRLHIVI.....KPRLAEKPSDHLPLVAVFDV 257

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 578766 seqs, 122855171 residues

Word size : 0

Total number of hits satisfying chosen parameters: 578766

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.